AMENDMENTS TO THE CLAIMS

Please cancel claims 15-21, 23-26, 29-32, 34-36, 38-40 and 43-44. A complete listing of the claims is set forth below.

1. (original) A method of identifying a cyclic peptide capable of altering a phenotype of a cell, comprising the step of:

administering to the cell a cyclic peptide comprising a chaperone binding region of known sequence and a target binding region of wholly or partially unknown sequence; and

assessing whether a phenotype of the cell has been altered.

2. (original) The method of Claim 1 in which the cyclic peptide is composed wholly of gene-encoded amino acids.

3. (original) The method of Claim 1 in which the chaperone binding region binds an imunophilin.

4. (original) The method of Claim 3 in which the immunophilin is cyclophilin or n FK-binding protein.

5. (original) The method of Claim 4 in which the cyclophilin is selected from the group consisting of cypA, cypB, and cycD.

6. (original) The method of Claim 4 in which the fK-binding protein is selected fromt eh group consisting of FKBP12, FKBP13, FKBP25, and FKBP59.

7. (original) The method of Claim 3 in which the immunophilin is endogenous to the cell.

8. (original) The method of Claim 3 in which the immunophilin is exogenous to the cell.

9. (original) The method of Claim 1 in which the chaperone binding region has an amino acid sequence selected from the group consisting of Ala-Gly-Pro-Ile and Leu-Pro.

10. (original) The method of Claim 1 further including the step of determining the sequence of the target binding region of the cyclic peptide.

11. (original) The method of Claim 1 in which the target binding region of the cyclic peptide is composed of from 4 to 10 amino acid residues.

12. (original) The method of Claim 1 in which the chaperone binding region and the target binding region of the cyclic peptide are contiguous.

13. (original) The method of Claim 1 in which the chaperone binding region and the target binding region of the cyclic peptide are spaced apart from one another via linkers, which may be the same or different.

14. (original) A method of identifying a cyclic peptide capable of altering a phenotype of a cell, comprising the steps of :

administering to a plurality of cells a plurality of cyclic peptides, each of which comprises a chaperone binding region and a target binding region;

identifying those cells exhibiting an altered phenotype (positive cells); and

determining the sequence of at least the target binding region of the cyclic peptides of positive cells.

15-21. (Cancelled)

22. (original) A method of isolating a target capable of altering a phenotype of a cell, comprising the steps of:

administering to a cell expressing a chaperone a cyclic peptide comprising a region capable of binding the chaperone and a target binding region of wholly or partially unknown sequence;

if the cell exhibits an altered phenotype, contacting a lysate of the cell with an affinity reagent capable of specifically binding a the chaperone; and

dissociating and isolating any target bound to the chaperone.

23-26. (Cancelled)

27. (original) A method of identifying a target capable of altering a phenotype of a cell, comprising the steps of:

administering to each of a plurality of cells a cyclic peptide comprising a chaperone binding region and a unique target binding region;

isolating a cell exhibiting an altered phenotype;

contacted said isolated cell with an affinity reagent that specifically binds the chaperone;

isolating there from any bound target; and

determining the identity of the isolated target.

28. (original) A cyclic peptide composed of from 4 to 30 amino acids, comprising:

a chaperone binding region; and

a target binding region of wholly or partially unknown sequence.

29-32. (Cancelled)

33. (original) A library of cyclic peptides, each of which comprises a chaperone binding region and a target binding region, wherein the target binding region of each cyclic peptide is unique.

34-36. (Cancelled)

37. (original) A polynucleotide capable of expressing a cyclic peptide comprising;

a first segment encoding a C-terminal intein domain;

a second segment encoding a linear version of cyclic peptide, said cyclic peptide comprising a chaperone binding region and a target binding region; and

a third segment encoding an N-terminal intein domain, wherein the first, second and third segments are arranged such that the polynucleotide expresses a cyclic peptide.

38-40. (Cancelled)

41. (original) A library of polynucleotides capable of expressing cyclic peptides, each polynucleotide of the library comprising:

a first segment encoding a C-terminal intein domain;

a second segment encoding a linear version of a cyclic peptide, said cyclic peptide comprising a chaperone binding region and a target binding region; and

a third segment encoding an N-terminal intein domain, wherein said first, second and third segments are arranged such that the ploynucleotide is capable of expressing the cyclic peptide and wherein the target binding region of each expressed cyclic peptide is unique.

42. (original) A host cell comprising a polynucleotide according to Claim 41, or progeny thereof.

43-44. (Cancelled)

Formal Matters

Claims 15-21, 23-26, 29-32, 34-36, 38-40 and 43-44 are cancelled without prejudice to renewal.

Claims 1-14, 22, 27, 28, 33, 37, 41 and 42 are pending.

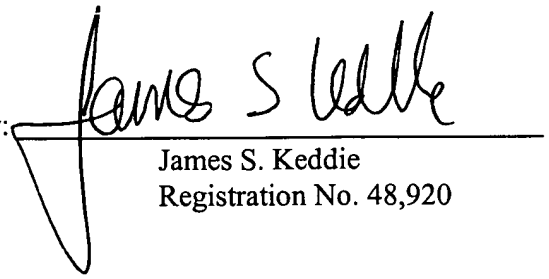
No new matter is added.

Examination of the pending claims is requested.

The Commissioner is authorized to charge any shortages of fees or credit any overages, to Deposit Account No. 50-0815 order number RIGL-023 (37 C.F.R. § 1.137(b)(2)).

Respectfully submitted,
BOZICEVIC, FIELD & FRANCIS LLP

Date: April 24, 2006

By: 

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